



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/817,431
Source: TFW
Date Processed by STIC: 4/8/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/817,431
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:49.

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

4 <110> APPLICANT: Degussa AG

7 <120> TITLE OF INVENTION: Process for the production of L-amino acids using strains of the

8 Enterobacteriaceae family

11 <130> FILE REFERENCE: 020489 BT

C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/817,431

C--> 14 <141> CURRENT FILING DATE: 2004-04-05

14 <160> NUMBER OF SEQ ID NOS: 8

17 <170> SOFTWARE: PatentIn version 3.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 30

22 <212> TYPE: DNA

23 <213> ORGANISM: Synthetic sequence

26 <220> FEATURE:

W--> 27 <221> NAME/KEY: Primer

28 <222> LOCATION: (1)..(30)

29 <223> OTHER INFORMATION: yfiD1

32 <220> FEATURE:

W--> 33 <221> NAME/KEY: Restriction site

34 <222> LOCATION: (9)..(14)

35 <223> OTHER INFORMATION: XbaI site

38 <400> SEQUENCE: 1

39 gaacaaatct agaaattaag ccgggggaggc

41 <210> SEQ ID NO: 2

42 <211> LENGTH: 24

43 <212> TYPE: DNA

44 <213> ORGANISM: Synthetic sequence

47 <220> FEATURE:

W--> 48 <221> NAME/KEY: Primer

49 <222> LOCATION: (1)..(24)

50 <223> OTHER INFORMATION: yfiD2

53 <220> FEATURE:

W--> 54 <221> NAME/KEY: Restriction site

55 <222> LOCATION: (8)..(13)

56 <223> OTHER INFORMATION: HindIII site

59 <400> SEQUENCE: 2

60 gctacttaag ctttacaggc tttc

62 <210> SEQ ID NO: 3

64 <211> LENGTH: 431

65 <212> TYPE: DNA

66 <213> ORGANISM: Escherichia coli

69 <220> FEATURE:

W--> 70 <221> NAME/KEY: yfiD PCR product

71 <222> LOCATION: (1)..(431)

Does Not Comply
Corrected Diskette Needed

Invalid
Response

mandatory <213> Response
has to be either Artificial
Unknown or Genus/Species,
Please see item #
10 on error summary
sheet.

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

72 <223> OTHER INFORMATION:

75 <220> FEATURE:

76 <221> NAME/KEY: CDS

77 <222> LOCATION: (36)..(419)

78 <223> OTHER INFORMATION: open reading frame yfiD

W--> 81 <400> 3

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82 gaacaaatct agaaattaag ccggggaggc atcac atg att aca ggt atc cag      53
83                               Met Ile Thr Gly Ile Gln
84                               1           5
86 att act aaa gcc gct aac gac gat ctg ctg aac tct ttc tgg ctg ctg      101
87 Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu Asn Ser Phe Trp Leu Leu
88           10           15           20
90 gac agc gaa aaa ggc gaa gcg cgt tgc atc gtt gca aaa gca ggt tat      149
91 Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile Val Ala Lys Ala Gly Tyr
92           25           30           35
94 gca gaa gat gaa gtg gtt gca gta agc aaa ctg ggt gac att gaa tac      197
95 Ala Glu Asp Glu Val Val Ala Val Ser Lys Leu Gly Asp Ile Glu Tyr
96           40           45           50
98 cgt gaa gtt cca gta gaa gtg aaa cca gaa gtt cgc gtt gaa ggt ggt      245
99 Arg Glu Val Pro Val Glu Val Lys Pro Glu Val Arg Val Glu Gly Gly
100 55           60           65           70
102 caa cac ctg aac gtt aac gtt ctg cgt cgc gaa act ctg gaa gat gca      293
103 Gln His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Glu Asp Ala
104           75           80           85
106 gtt aag cat ccg gaa aaa tat ccg cag ctg acc atc cgt gta tcc ggt      341
107 Val Lys His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly
108           90           95           100
110 tat gca gtt cgc ttt aac tct ctg act ccg gaa cag cag cgc gac gtt      389
111 Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val
112           105           110           115
114 atc gct cgt acc ttt act gaa agc ctg taa agcttaagta gc      431
115 Ile Ala Arg Thr Phe Thr Glu Ser Leu
116           120           125
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 127
121 <212> TYPE: PRT
122 <213> ORGANISM: Escherichia coli
125 <400> SEQUENCE: 4
126 Met Ile Thr Gly Ile Gln Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu
127 1           5           10           15
129 Asn Ser Phe Trp Leu Leu Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile
130           20           25           30
132 Val Ala Lys Ala Gly Tyr Ala Glu Asp Glu Val Val Ala Val Ser Lys
133           35           40           45
135 Leu Gly Asp Ile Glu Tyr Arg Glu Val Pro Val Glu Val Lys Pro Glu
136           50           55           60
138 Val Arg Val Glu Gly Gly Gln His Leu Asn Val Asn Val Leu Arg Arg
139 65           70           75           80
141 Glu Thr Leu Glu Asp Ala Val Lys His Pro Glu Lys Tyr Pro Gln Leu

```

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

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142                85                90                95
144 Thr Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro
145                100                105                110
147 Glu Gln Gln Arg Asp Val Ile Ala Arg Thr Phe Thr Glu Ser Leu
148                115                120                125
150 <210> SEQ ID NO: 5
151 <211> LENGTH: 28
152 <212> TYPE: DNA
153 <213> ORGANISM: Synthetic sequence
156 <220> FEATURE:
W--> 157 <221> NAME/KEY: Primer
158 <222> LOCATION: (1)..(28)
159 <223> OTHER INFORMATION: pflB1
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: Restriction site
164 <222> LOCATION: (5)..(10)
165 <223> OTHER INFORMATION: XbaI site
168 <400> SEQUENCE: 5
169 ccactctaga aggtaggtgt tacatgtc
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Synthetic sequence
177 <220> FEATURE:
W--> 178 <221> NAME/KEY: Primer
179 <222> LOCATION: (1)..(27)
180 <223> OTHER INFORMATION: pflB2
183 <220> FEATURE:
W--> 184 <221> NAME/KEY: Restriction site
185 <222> LOCATION: (13)..(18)
186 <223> OTHER INFORMATION: HindIII site
189 <400> SEQUENCE: 6
190 cgatttcagt caaagcttat tacatag
193 <210> SEQ ID NO: 7
194 <211> LENGTH: 2325
195 <212> TYPE: DNA
196 <213> ORGANISM: Escherichia coli
199 <220> FEATURE:
W--> 200 <221> NAME/KEY: pflB PCR product
201 <222> LOCATION: (1)..(2325)
202 <223> OTHER INFORMATION:
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (24)..(2306)
208 <223> OTHER INFORMATION: pflB coding region
W--> 211 <400> 7
212 ccactctaga aggtaggtgt tac atg tcc gag ctt aat gaa aag tta gcc aca
213                Met Ser Glu Leu Asn Glu Lys Leu Ala Thr
214                1                5                10

```

28

27

53

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\SEQUENCE LISTING.txt

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```

216 gcc tgg gaa ggt ttt acc aaa ggt gac tgg cag aat gaa 'gta aac gtc      101
217 Ala Trp Glu Gly Phe Thr Lys Gly Asp Trp Gln Asn Glu Val Asn Val
218              15              20              25
220 cgt gac ttc att cag aaa aac tac act ccg tac gag ggt gac gag tcc      149
221 Arg Asp Phe Ile Gln Lys Asn Tyr Thr Pro Tyr Glu Gly Asp Glu Ser
222              30              35              40
224 ttc ctg gct ggc gct act gaa gcg acc acc acc ctg tgg gac aaa gta      197
225 Phe Leu Ala Gly Ala Thr Glu Ala Thr Thr Thr Leu Trp Asp Lys Val
226              45              50              55
228 atg gaa ggc gtt aaa ctg gaa aac cgc act cac gcg cca gtt gac ttt      245
229 Met Glu Gly Val Lys Leu Glu Asn Arg Thr His Ala Pro Val Asp Phe
230              60              65              70
232 gac acc gct gtt gct tcc acc atc acc tct cac gac gct ggc tac atc      293
233 Asp Thr Ala Val Ala Ser Thr Ile Thr Ser His Asp Ala Gly Tyr Ile
234 75              80              85              90
236 aac aag cag ctt gag aaa atc gtt ggt ctg cag act gaa gct ccg ctg      341
237 Asn Lys Gln Leu Glu Lys Ile Val Gly Leu Gln Thr Glu Ala Pro Leu
238              95              100              105
240 aaa cgt gct ctt atc ccg ttc ggt ggt atc aaa atg atc gaa ggt tcc      389
241 Lys Arg Ala Leu Ile Pro Phe Gly Gly Ile Lys Met Ile Glu Gly Ser
242              110              115              120
244 tgc aaa gcg tac aac cgc gaa ctg gat ccg atg atc aaa aaa atc ttc      437
245 Cys Lys Ala Tyr Asn Arg Glu Leu Asp Pro Met Ile Lys Lys Ile Phe
246              125              130              135
248 act gaa tac cgt aaa act cac aac cag ggc gtg ttc gac gtt tac act      485
249 Thr Glu Tyr Arg Lys Thr His Asn Gln Gly Val Phe Asp Val Tyr Thr
250              140              145              150
252 ccg gac atc ctg cgt tgc cgt aaa tct ggt gtt ctg acc ggt ctg cca      533
253 Pro Asp Ile Leu Arg Cys Arg Lys Ser Gly Val Leu Thr Gly Leu Pro
254 155              160              165              170
256 gat gca tat ggc cgt ggc cgt atc atc ggt gac tac cgt cgc gtt gcg      581
257 Asp Ala Tyr Gly Arg Gly Arg Ile Ile Gly Asp Tyr Arg Arg Val Ala
258              175              180              185
260 ctg tac ggt atc gac tac ctg atg aaa gac aaa ctg gca cag ttc act      629
261 Leu Tyr Gly Ile Asp Tyr Leu Met Lys Asp Lys Leu Ala Gln Phe Thr
262              190              195              200
264 tct ctg cag gct gat ctg gaa aac ggc gta aac ctg gaa cag act atc      677
265 Ser Leu Gln Ala Asp Leu Glu Asn Gly Val Asn Leu Glu Gln Thr Ile
266              205              210              215
268 cgt ctg cgc gaa gaa atc gct gaa cag cac cgc gct ctg ggt cag atg      725
269 Arg Leu Arg Glu Glu Ile Ala Glu Gln His Arg Ala Leu Gly Gln Met
270              220              225              230
272 aaa gaa atg gct gcg aaa tac ggc tac gac atc tct ggt ccg gct acc      773
273 Lys Glu Met Ala Ala Lys Tyr Gly Tyr Asp Ile Ser Gly Pro Ala Thr
274 235              240              245              250
276 aac gct cag gaa gct atc cag tgg act tac ttc ggc tac ctg gct gct      821
277 Asn Ala Gln Glu Ala Ile Gln Trp Thr Tyr Phe Gly Tyr Leu Ala Ala
278              255              260              265
280 gtt aag tct cag aac ggt gct gca atg tcc ttc ggt cgt acc tcc acc      869

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Output Set: N:\CRF4\04082004\J817431.raw

281	Val	Lys	Ser	Gln	Asn	Gly	Ala	Ala	Met	Ser	Phe	Gly	Arg	Thr	Ser	Thr		
282				270					275					280				
284	ttc	ctg	gat	gtg	tac	atc	gaa	cgt	gac	ctg	aaa	gct	ggc	aag	atc	acc	917	
285	Phe	Leu	Asp	Val	Tyr	Ile	Glu	Arg	Asp	Leu	Lys	Ala	Gly	Lys	Ile	Thr		
286			285					290					295					
288	gaa	caa	gaa	gcg	cag	gaa	atg	ggt	gac	cac	ctg	gtc	atg	aaa	ctg	cgt	965	
289	Glu	Gln	Glu	Ala	Gln	Glu	Met	Val	Asp	His	Leu	Val	Met	Lys	Leu	Arg		
290		300					305					310						
292	atg	ggt	cgc	ttc	ctg	cgt	act	ccg	gaa	tac	gat	gaa	ctg	ttc	tct	ggc	1013	
293	Met	Val	Arg	Phe	Leu	Arg	Thr	Pro	Glu	Tyr	Asp	Glu	Leu	Phe	Ser	Gly		
294	315				320				325						330			
296	gac	ccg	atc	tgg	gca	acc	gaa	tct	atc	ggg	ggg	atg	ggc	ctc	gac	ggg	1061	
297	Asp	Pro	Ile	Trp	Ala	Thr	Glu	Ser	Ile	Gly	Gly	Met	Gly	Leu	Asp	Gly		
298				335					340					345				
300	cgt	acc	ctg	ggt	acc	aaa	aac	agc	ttc	cgt	ttc	ctg	aac	acc	ctg	tac	1109	
301	Arg	Thr	Leu	Val	Thr	Lys	Asn	Ser	Phe	Arg	Phe	Leu	Asn	Thr	Leu	Tyr		
302			350						355					360				
304	acc	atg	ggg	ccg	tct	ccg	gaa	ccg	aac	atg	acc	att	ctg	tgg	tct	gaa	1157	
305	Thr	Met	Gly	Pro	Ser	Pro	Glu	Pro	Asn	Met	Thr	Ile	Leu	Trp	Ser	Glu		
306			365					370					375					
308	aaa	ctg	ccg	ctg	aac	ttc	aag	aaa	ttc	gcc	gct	aaa	gtg	tcc	atc	gac	1205	
309	Lys	Leu	Pro	Leu	Asn	Phe	Lys	Lys	Phe	Ala	Ala	Lys	Val	Ser	Ile	Asp		
310		380			385				390									
312	acc	tct	tct	ctg	cag	tat	gag	aac	gat	gac	ctg	atg	cgt	ccg	gac	ttc	1253	
313	Thr	Ser	Ser	Leu	Gln	Tyr	Glu	Asn	Asp	Asp	Leu	Met	Arg	Pro	Asp	Phe		
314	395				400				405						410			
316	aac	aac	gat	gac	tac	gct	att	gct	tgc	tgc	gta	agc	ccg	atg	atc	ggt	1301	
317	Asn	Asn	Asp	Asp	Tyr	Ala	Ile	Ala	Cys	Cys	Val	Ser	Pro	Met	Ile	Val		
318				415					420					425				
320	ggg	aaa	caa	atg	cag	ttc	ttc	ggg	gag	cgt	gca	aac	ctg	gag	aaa	acc	1349	
321	Gly	Lys	Gln	Met	Gln	Phe	Phe	Gly	Ala	Arg	Ala	Asn	Leu	Ala	Lys	Thr		
322			430					435					440					
324	atg	ctg	tac	gca	atc	aac	ggc	ggc	ggt	gac	gaa	aaa	ctg	aaa	atg	cag	1397	
325	Met	Leu	Tyr	Ala	Ile	Asn	Gly	Gly	Val	Asp	Glu	Lys	Leu	Lys	Met	Gln		
326			445				450						455					
328	ggt	ggg	ccg	aag	tct	gaa	ccg	atc	aaa	ggc	gat	gtc	ctg	aac	tat	gat	1445	
329	Val	Gly	Pro	Lys	Ser	Glu	Pro	Ile	Lys	Gly	Asp	Val	Leu	Asn	Tyr	Asp		
330		460					465					470						
332	gaa	gtg	atg	gag	cgc	atg	gat	cac	ttc	atg	gac	tgg	ctg	gct	aaa	cag	1493	
333	Glu	Val	Met	Glu	Arg	Met	Asp	His	Phe	Met	Asp	Trp	Leu	Ala	Lys	Gln		
334	475				480				485						490			
336	tac	atc	act	gca	ctg	aac	atc	atc	cac	tac	atg	cac	gac	aag	tac	agc	1541	
337	Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Ile	His	Tyr	Met	His	Asp	Lys	Tyr	Ser		
338				495					500					505				
340	tac	gaa	gcc	tct	ctg	atg	gag	ctg	cac	gac	cgt	gac	ggt	atc	cgc	acc	1589	
341	Tyr	Glu	Ala	Ser	Leu	Met	Ala	Leu	His	Asp	Arg	Asp	Val	Ile	Arg	Thr		
342			510					515					520					
344	atg	gag	tgt	ggg	atc	gct	ggg	ctg	tcc	ggt	gct	gct	gac	tcc	ctg	tct	1637	
345	Met	Ala	Cys	Gly	Ile	Ala	Gly	Leu	Ser	Val	Ala	Ala	Asp	Ser	Leu	Ser		

VERIFICATION SUMMARY

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:50

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:81 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:72
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:202